

Robinson



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/659,379

DATE: 02/11/2003

TIME: 20:10:26

Input Set : N:\Crf3\RULE60\09659379.txt

Output Set: N:\CRF4\02112003\I659379.raw

SEQUENCE LISTING**ENTERED**

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Vinik, Aaron
 6 Pittenger, Gary
 7 Rafaeloff-Phail, Ronit
 8 Barlow, Scott

10 (ii) TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
 11 INGAP IN BACTERIAL AND EUKARYOTIC CELLS

13 (iii) NUMBER OF SEQUENCES: 6

15 (iv) CORRESPONDENCE ADDRESS:
 16 (A) ADDRESSEE: Banner & Witcoff, Ltd.
 17 (B) STREET: 1001 G Street, N.W.
 18 (C) CITY: Washington
 19 (D) STATE: DC
 20 (E) COUNTRY: USA
 21 (F) ZIP: 20001

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Diskette
 25 (B) COMPUTER: IBM Compatible
 26 (C) OPERATING SYSTEM: DOS
 27 (D) SOFTWARE: FastSEQ for Windows Version 2.0

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/659,379
 C--> 31 (B) FILING DATE: 08-Sep-2000

32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

W--> 35 (A) APPLICATION NUMBER: US/08/909,725
 36 (B) FILING DATE: 12-AUG-1997

W--> 37 (A) APPLICATION NUMBER: 08/741,096
 38 (B) FILING DATE: 30-OCT-1996

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Kagan, Sarah A
 44 (B) REGISTRATION NUMBER: 32,145
 45 (C) REFERENCE/DOCKET NUMBER: 0570.05173

47 (ix) TELECOMMUNICATION INFORMATION:
 48 (A) TELEPHONE: 202-508-9100

49 (B) TELEFAX: 202-508-9299
 50 (C) TELEX: 97430 BMB UT

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:
 56 (A) LENGTH: 94 base pairs
 57 (B) TYPE: nucleic acid
 58 (C) STRANDEDNESS: single

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59	(D) TOPOLOGY: linear	
62	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
64	CTGCAAGACA GGTACCATGA TGCTTCCCCT GACCCTCTGT AGGATGTCTT GGATGCTGCT	60
65	TTCCTGCCTG ATGTTCCCTT CTTGGGTGGA AGGT	94
67	(2) INFORMATION FOR SEQ ID NO: 2:	
69	(i) SEQUENCE CHARACTERISTICS:	
70	(A) LENGTH: 31 base pairs	
71	(B) TYPE: nucleic acid	
72	(C) STRANDEDNESS: single	
73	(D) TOPOLOGY: linear	
76	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
78	CCGC GGATCC CGAAGAATCT CAAAAGAAAC T	31
80	(2) INFORMATION FOR SEQ ID NO: 3:	
82	(i) SEQUENCE CHARACTERISTICS:	
83	(A) LENGTH: 32 base pairs	
84	(B) TYPE: nucleic acid	
85	(C) STRANDEDNESS: single	
86	(D) TOPOLOGY: linear	
89	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
91	GACCGGGCTCG AGTGCTCTTC CTGAGTGAAT CC	32
93	(2) INFORMATION FOR SEQ ID NO: 4:	
95	(i) SEQUENCE CHARACTERISTICS:	
96	(A) LENGTH: 558 base pairs	
97	(B) TYPE: nucleic acid	
98	(C) STRANDEDNESS: single	
99	(D) TOPOLOGY: linear	
101	(ii) MOLECULE TYPE: cDNA	
103	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
105	CCGC GGATCC CGAAGAATCT CAAAAGAAAC TGCTTCTTC ACGTATAACC TGT CCTCAAG	60
106	GCTCTGTAGC CTATGGGTCC TATTGCTATT CACTGATTGTT GATACCACAG ACCTGGTCTA	120
107	ATGCAGAACT ATCCTGCCAG ATGCATTCT CAGGACACCT GGCATTCTT CTCAGTACTG	180
108	GTGAAATTAC CTTCGTGTCC TCCCTGTGA AGAACAGTTT GACGGCCTAC CAGTACATCT	240
109	GGATTGGACT CCATGATCCC TCACATGGTA CACTACCAA CGGAAGTGGA TGGAAAGTGGA	300
110	GCAGTTCCAA TGTGCTGACC TTCTATAACT GGGAGAGGAA CCCCTCTATT GCTGCTGACC	360
111	GTGGTTATTG TGCAGTTTG TCTCAGAAAT CAGGTTTCA GAAGTGGAGA GATTTAATT	420
112	GTGAAAATGA GCTTCCCTAT ATCTGCAAAT TCAAGGTCTA GGGCAGTTCT AATTCACA	480
113	GCTTGAAAAT ATTATGAAGC TCACATGGAC AAGGAAGCAA GTATGAGGAT TCACTCAGGA	540
114	AGAGCACTCG AGCCGGTC	558
116	(2) INFORMATION FOR SEQ ID NO: 5:	
118	(i) SEQUENCE CHARACTERISTICS:	
119	(A) LENGTH: 26 amino acids	
120	(B) TYPE: amino acid	
121	(C) STRANDEDNESS: single	
122	(D) TOPOLOGY: linear	
124	(ii) MOLECULE TYPE: peptide	
126	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
128	Met Met Leu Pro Met Thr Leu Cys Arg Met Ser Trp Met Leu Leu Ser	
129	1 5 10 15	
130	Cys Leu Met Phe Leu Ser Trp Val Glu Gly	

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131 20 25
133 (2) INFORMATION FOR SEQ ID NO: 6:
135 (i) SEQUENCE CHARACTERISTICS:
136 (A) LENGTH: 175 amino acids
137 (B) TYPE: amino acid
138 (C) STRANDEDNESS: single
139 (D) TOPOLOGY: linear
141 (ii) MOLECULE TYPE: protein
143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
145 Met Met Leu Pro Met Thr Leu Cys Arg Met Ser Trp Met Leu Leu Ser
146 1 5 10 15
147 Cys Leu Met Phe Leu Ser Trp Val Glu Gly Glu Glu Ser Gln Lys Lys
148 20 25 30
149 Leu Pro Ser Ser Arg Ile Thr Cys Pro Gln Gly Ser Val Ala Tyr Gly
150 35 40 45
151 Ser Tyr Cys Tyr Ser Leu Ile Leu Ile Pro Gln Thr Trp Ser Asn Ala
152 50 55 60
153 Glu Leu Ser Cys Gln Met His Phe Ser Gly His Leu Ala Phe Leu Leu
154 65 70 75 80
155 Ser Thr Gly Glu Ile Thr Phe Val Ser Ser Leu Val Lys Asn Ser Leu
156 85 90 95
157 Thr Ala Tyr Gln Tyr Ile Trp Ile Gly Leu His Asp Pro Ser His Gly
158 100 105 110
159 Thr Leu Pro Asn Gly Ser Gly Trp Lys Trp Ser Ser Ser Asn Val Leu
160 115 120 125
161 Thr Phe Tyr Asn Trp Glu Arg Asn Pro Ser Ile Ala Ala Asp Arg Gly
162 130 135 140
163 Tyr Cys Ala Val Leu Ser Gln Lys Ser Gly Phe Gln Lys Trp Arg Asp
164 145 150 155 160
165 Phe Asn Cys Glu Asn Glu Leu Pro Tyr Ile Cys Lys Phe Lys Val
166 165 170 175

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:37 M:238 W: Alpha Fields not Ordered [(A) APPLICATION NUMBER:] of (1) (vii)